

SEQUENCE LISTING

<110> Cohen, Bruce D.  
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Gallo, Michael

<120> ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR

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<150> 60/259, 927  
<151> 2001-01-05

<160> 60

<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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ccgttacaa agtggggtcc catcaagggtt cagcggcagt ggatctggaa cagaattcac 180  
tctcacaatc agcagcctgc agcctgaaga ttttgcact tattactgtc tacagcataa 240  
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<213> Homo sapiens

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20 25 30

Lys Arg Leu Ile Tyr Ala Ala Ser Arg Leu Gln Ser Gly Val Pro Ser  
35 40 45

Arg Phe Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser  
50 55 60

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn  
65 70 75 80

Asn Tyr Pro Arg Thr Phe Gly Gln Gly Thr Glu Val Glu Ile Ile Arg  
85 90 95

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
100 105 110

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<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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20 25 30

Pro Gly Lys Gly Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Gly Ser  
35 40 45

Thr Arg Asp Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg  
50 55 60

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala  
65 70 75 80

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg Asp Gly Val Glu Thr Thr  
85 90 95

Phe Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr  
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
115 120 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys  
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
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Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ser Cys Ala  
165 170

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<213> Homo sapiens

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp  
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile  
35 40 45

Tyr Ala Ala Ser Arg Leu His Arg Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Cys  
85 90 95

Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

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20 25 30

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
35 40 45

Ala Ile Ser Gly Ser Gly Gly Thr Thr Phe Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Thr Thr Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Lys Asp Leu Gly Trp Ser Asp Ser Tyr Tyr Tyr Tyr Gly Met Asp  
100 105 110

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acagaattca ctctcacaat cagcagcctg cagcctgaag attttgcaac ttattactgt 240  
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<213> Homo sapiens

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Ala Ser Gln Asp Ile Arg Arg Asp Leu Gly Trp Tyr Gln Gln Lys Pro  
20 25 30

Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Arg Leu Gln Ser

35

40

45

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr  
50 55 60

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys  
65 70 75 80

Leu Gln His Asn Asn Tyr Pro Arg Thr Phe Gly Gln Gly Thr Glu Val  
85 90 95

Glu Ile Ile Arg  
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<211> 338

<212> DNA

<213> Homo sapiens

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gattgggggt atctatacca gtgggagccc caactacaac ccctccctca agagtcgagt 180  
caccatgtca gtagacacgt ccaagaacca gttctccctg aagctgaact ctgtgacccg 240  
cgccggacacg gccgtgtatt actgtgcggt aacgatttt ggagtggta ttatcttga 300  
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<211> 112

<212> PRT

<213> Homo sapiens

<400> 12

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20 25 30

Pro Ala Gly Lys Gly Leu Glu Trp Ile Gly Arg Ile Tyr Thr Ser Gly  
35 40 45

Ser Pro Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Ser Val  
50 55 60

Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Asn Ser Val Thr Ala  
65 70 75 80

Ala Asp Thr Ala Val Tyr Tyr Cys Ala Val Thr Ile Phe Gly Val Val  
85 90 95

Ile Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
100 105 110

<210> 13

<211> 322

<212> DNA

<213> Homo sapiens

<400> 13

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gggaaagccc ctaagcgct gatctatgct gcatccaaat tacaccgtgg ggtccccatca 180  
aggttcagcg gcagtggatc tgggacagaa ttcaactctca caatcagccg cctgcagcct 240  
gaagattttgc caacttattt ctgtctacag cataatagtt accctctcac tttcggcgga 300  
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<210> 14

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<212> PRT

<213> Homo sapiens

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Ser Asp  
20 25 30

Leu Gly Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile  
35 40 45

Tyr Ala Ala Ser Lys Leu His Arg Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Arg Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu  
85 90 95

Thr Phe Gly Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 15

<211> 376

<212> DNA

<213> Homo sapiens

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ccagggaaagg ggctggaggc ggtctcagct attagttggta gtgggtgtat cacataactac 180  
gcagactccg tgaaggggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgc当地atc acagcctgag agccgaggac acggccgtat attactgtgc gaaagatctg 300  
ggctacggtg acttttacta ctactactac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctcag 376

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<212> PRT

<213> Homo sapiens

<400> 16

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Asp Leu Gly Tyr Gly Asp Phe Tyr Tyr Tyr Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 17

<211> 279

<212> DNA

<213> Homo sapiens

<400> 17

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aagggtgggtt cccatcaagg ttcatggca gtggatctgg gacagatttc actctcacca 180  
tcagcagtct gcaacactgaa gattttgcaa cttaactactg tcaacagagt tacaatgccc 240  
cactcaactt cggcgaggacc accaagggtgg agatcaaac 279

<210> 18

<211> 92

<212> PRT

<213> Homo sapiens

<400> 18

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr  
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Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu  
20 25 30

Ile His Val Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser  
35 40 45

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln  
50 55 60

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Ala Pro  
65 70 75 80

Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys

85

90

<210> 19  
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catatcagta gacacgtcca agaaccagt ctccctgaag ctgagttctg tgaccgctgc 240  
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<211> 113  
<212> PRT  
<213> Homo sapiens  
  
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Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val  
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Ser Gly Gly Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro  
20 25 30  
Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser  
35 40 45  
Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp  
50 55 60  
Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala  
65 70 75 80  
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Thr Tyr Ser Ser Ser Phe Tyr  
85 90 95  
Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser  
100 105 110  
Ser

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<211> 274  
<212> DNA  
<213> Homo sapiens  
  
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<223> a, c, t, g, other or unknown  
  
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ggcatcccag acaggttcag tggcagtggg tctgggacag acttcactct caccatcagc 180  
agactggagc ctgaagattt tgcaagtgtt tactgtcagc agtatggtag ttcacctcgn 240  
acgttcgcc aagggaccaa ggtggaaatc aaac 274

<210> 22  
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<400> 22  
Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Gly Arg Tyr  
1 5 10 15  
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
20 25 30  
Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly  
35 40 45  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro  
50 55 60  
Glu Asp Phe Ala Val Phe Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Arg  
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
85 90

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<212> DNA  
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ccagggagg ggctggagtg ggtctcaggt attactggg a t g g t g g t a g t a c a t a c a t a c 180  
gcagactccg tgaaggccg gttcaccatc tccagagaca attccaagaa c a c g c t g t a t 240  
ctgcaa atga acagcctgag agccgaggac acggccgtat attactgtgc gaaagatcca 300  
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tcctcag 367

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<212> PRT  
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20 25 30  
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Asp Pro Gly Thr Thr Val Ile Met Ser Trp Phe Asp Pro Trp  
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 25

<211> 320

<212> DNA

<213> Homo sapiens

<400> 25

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ggaagggtgga taacgcctc caatcggta actcccagga gagtgtcaca gagcaggaca 180  
gcaaggacag cacctacagc ctcagcagca ccctgacgct gagcaaagca gactacgaga 240  
aacacaaaagt ctacgcctgc gaagtcaccc atcagggcct gagctcgccc gtcacaaaaga 300  
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<210> 26

<211> 106

<212> PRT

<213> Homo sapiens

<400> 26

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
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20 25 30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
35 40 45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
50 55 60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
65 70 75 80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
85 90 95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
100 105

<210> 27

<211> 978

<212> DNA  
<213> Homo sapiens

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tacacctgca acgttagatca caagcccgac aacaccaagg tggacaagac agttgagcgc 300  
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aaggcttcca acaaaggctc cccagccccc atcgagaaaa ccatactccaa aaccaaagg 660  
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<210> 28  
<211> 326  
<212> PRT  
<213> Homo sapiens

<400> 28  
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Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
35 40 45  
  
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
50 55 60  
  
Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr  
65 70 75 80  
  
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
85 90 95  
  
Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
100 105 110  
  
Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
115 120 125  
  
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
130 135 140  
  
Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly  
145 150 155 160  
  
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn

165	170	175
Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp		
180	185	190
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro		
195	200	205
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu		
210	215	220
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn		
225	230	235
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile		
245	250	255
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr		
260	265	270
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys		
275	280	285
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys		
290	295	300
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu		
305	310	315
Ser Leu Ser Pro Gly Lys		
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gcagactctg tgaaggcccg attcaccatc tccagggaca acgccaagaa ctcactgtat 240		
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr		
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Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
35	40	45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg

<210> 31

<211> 296

<212> DNA

<213> Homo sapiens

<400> 31

gaggtgcagc tgggggaggc ttggtagacgc ctggggggtc cctgagactc 60  
tcctgtgcag cctctggatt cacctttagc agctatgcc a tgagctgggt ccggccaggct 120  
ccagggaaagg ggctggaggc ggtctcagct attagtggta gtggtggtag cacataactac 180  
gcagactccg tgaaggggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaga 296

<210> 32

<211> 98

<212> PRT

<213> Homo sapiens

<400> 32

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys

<210> 33

<211> 296

<212> DNA

<213> Homo sapiens

<400> 33

caggtgcagc tgcaggagtc gggcccaagga ctggtaaagc cttcgggac cctgtccctc 60

acctgcgctg tctctgggg ctccatcagc agtagtaact ggtggagttg ggtcccccag 120  
cccccaggaa aggggctgga gtggattggg gaaatctatc atagtgggag caccaactac 180  
aaccctgtccc tcaagagtcg agtaccata tcagtagaca agtccaagaa ccagttctcc 240  
ctgaagctga gctctgtac cgccgcggac acggccgtgt attactgtgc gagaga 296

<210> 34  
<211> 98  
<212> PRT  
<213> Homo sapiens

<400> 34  
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser  
20 25 30

Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp  
35 40 45

Ile Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu  
50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Lys Ser Lys Asn Gln Phe Ser  
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg

<210> 35  
<211> 293  
<212> DNA  
<213> Homo sapiens

<400> 35

caggtgcagc tgcaggagtc gggccagga ctggtaagc cttcgagac cctgtccctc 60  
acctgcactg tctctgggg ctccatcagt agttactact ggagctggat ccggcagccc 120  
ccagggaaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180  
ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgccggacacg gccgtgtatt actgtgcgag aga 293

<210> 36  
<211> 97  
<212> PRT  
<213> Homo sapiens

<400> 36

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg

<210> 37

<211> 290

<212> DNA

<213> Homo sapiens

<400> 37

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120  
cctggccagg cttccaggtct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatca gagactggag 240  
cctgaagatt ttgcagtgtta ttactgttag cagtatggta gtcacacctcc 290

<210> 38

<211> 96

<212> PRT

<213> Homo sapiens

<400> 38

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

<210> 39

<211> 288

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (288)

<223> a, c, t, g, other or unknown

<400> 39  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtacc 60  
atcaattgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120  
gggaaagccc ctaagcgct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagcg gcagtggatc tgggacagaa ttcaactctca caatcagcag cctgcagcct 240  
gaagatttttcaacttatta ctgtctacag cataatacgat accctccn 288

<210> 40  
<211> 96  
<212> PRT  
<213> Homo sapiens

<400> 40  
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp  
20 25 30  
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile  
35 40 45  
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60  
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80  
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro  
85 90 95

<210> 41  
<211> 288  
<212> DNA  
<213> Homo sapiens

<400> 41  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtacc 60  
atcaattgcc gggcaagtca gagcattagc agctattaa attggtatca gcagaaacca 120  
gggaaagccc ctaagctct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcaactctca ccatacagcag tctgcaacct 240  
gaagatttttcaacttacta ctgtcaacag agttacagta cccctccn 288

<210> 42  
<211> 96  
<212> PRT  
<213> Homo sapiens

<400> 42  
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr  
20 25 30  
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
16

35

40

45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro  
85 90 95

<210> 43

<211> 293

<212> DNA

<213> Homo sapiens

<400> 43

caggtgcagc tgcaggagtc gggcccgagga ctggtaaagc cttcgagac cctgtccctc 60  
acctgcactg tctctgggg ctccatcaat agttaactat ggagctggat ccggcagccc 120  
gccggaaagg gactggatgg gattgggggt atctatacca gtggggagcac caactacaac 180  
ccctccctca agagtcgatg caccatgtca gttagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc cgccggacacg gcccgtgtatt actgtgcgag aga 293

<210> 44

<211> 97

<212> PRT

<213> Homo sapiens

<400> 44

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Arg Ile Tyr Thr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg

<210> 45

<211> 470

<212> PRT

<213> Homo sapiens

<400> 45

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly  
1 5 10 15

Val	Gln	Cys	Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln
				20				25					30		
Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Thr	Phe
				35			40		45						
Ser	Ser	Tyr	Ala	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
				50			55		60						
Glu	Trp	Val	Ser	Ala	Ile	Ser	Gly	Ser	Gly	Gly	Thr	Thr	Phe	Tyr	Ala
				65			70		75		80				
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Arg	Thr
				85				90		95					
Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val
				100				105		110					
Tyr	Tyr	Cys	Ala	Lys	Asp	Leu	Gly	Trp	Ser	Asp	Ser	Tyr	Tyr	Tyr	Tyr
				115			120		125						
Tyr	Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
				130			135		140						
Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg
				145			150		155		160				
Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
				165				170		175					
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
				180				185		190					
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
				195				200		205		205			
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Asn	Phe	Gly	Thr	Gln	Thr
				210			215		220						
Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
				225			230		235		240				
Thr	Val	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro
				245				250		255					
Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp
				260			265		270						
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
				275				280		285					
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly
				290			295		300						
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn
				305			310		315		320				
Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp
				325				330		335					

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro  
340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu  
355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
405 410 415

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
450 455 460

Ser Leu Ser Pro Gly Lys  
465 470

<210> 46  
<211> 470  
<212> PRT  
<213> Homo sapiens

<400> 46  
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly  
1 5 10 15

Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Leu Val Gln  
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala  
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn  
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Lys Gly Tyr Ser Ser Gly Trp Tyr Tyr Tyr Tyr Tyr  
115 120 125

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

130	135	140
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg		
145	150	155
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr		
165	170	175
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser		
180	185	190
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser		
195	200	205
Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr		
210	215	220
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys		
225	230	235
Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro		
245	250	255
Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp		
260	265	270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp		
275	280	285
Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly		
290	295	300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn		
305	310	315
Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp		
325	330	335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro		
340	345	350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu		
355	360	365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn		
370	375	380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile		
385	390	395
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr		
405	410	415
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys		
420	425	430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys		
435	440	445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu		

450

455

460

Ser Leu Ser Pro Gly Lys  
465 470

<210> 47  
<211> 236  
<212> PRT  
<213> Homo sapiens

<400> 47  
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp  
1 5 10 15

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Phe Pro Ser Ser  
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
35 40 45

Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys  
50 55 60

Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Arg Leu His Arg Gly Val  
65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr  
85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln  
100 105 110

His Asn Ser Tyr Pro Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile  
115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

<210> 48  
<211> 236

<212> PRT

<213> Homo sapiens

<400> 48

Met	Asp	Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Trp	
1				5				10						15	
Phe	Pro	Gly	Ala	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser
	20							25						30	
Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser
	35							40						45	
Gln	Gly	Ile	Arg	Asn	Asp	Leu	Gly	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys
	50					55					60				
Ala	Pro	Lys	Arg	Leu	Ile	Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val
	65				70				75						80
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr
		85					90								95
Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln
		100					105							110	
His	Asn	Ser	Tyr	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile
		115				120						125			
Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp
	130					135					140				
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn
	145				150					155					160
Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu
		165						170						175	
Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp
		180					185						190		
Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr
		195				200					205				
Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser
	210				215					220					
Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
	225					230				235					

<210> 49

<211> 470

<212> PRT

<213> Homo sapiens

<400> 49

Met	Glu	Phe	Gly	Leu	Ser	Trp	Val	Phe	Leu	Val	Ala	Ile	Ile	Lys	Gly
1				5				10						15	

Val Gln Cys Gln Ala Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys

20	25	30
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe		
35	40	45
Ser Asp Tyr Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu		
50	55	60
Glu Trp Val Ser Tyr Ile Ser Ser Ser Gly Ser Thr Arg Asp Tyr Ala		
65	70	75
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn		
85	90	95
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val		
100	105	110
Tyr Tyr Cys Val Arg Asp Gly Val Glu Thr Thr Phe Tyr Tyr Tyr Tyr		
115	120	125
Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser		
130	135	140
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg		
145	150	155
160		
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr		
165	170	175
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser		
180	185	190
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser		
195	200	205
Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr		
210	215	220
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys		
225	230	235
240		
Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro		
245	250	255
Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp		
260	265	270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp		
275	280	285
Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly		
290	295	300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn		
305	310	315
320		
Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp		
325	330	335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro		

340	345	350	
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu 355	360	365	
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn 370	375	380	
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile 385	390	395	400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr 405	410	415	
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys 420	425	430	
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys 435	440	445	
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu 450	455	460	
Ser Leu Ser Pro Gly Lys 465	470		
<210> 50			
<211> 473			
<212> PRT			
<213> Homo sapiens			
<400> 50			
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Ile Lys Gly 1	5	10	15
Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Leu Val Lys 20	25	30	
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe 35	40	45	
Ser Asp Tyr Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu 50	55	60	
Glu Trp Val Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala 65	70	75	80
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn 85	90	95	
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val 100	105	110	
Tyr Tyr Cys Ala Arg Val Leu Arg Phe Leu Glu Trp Leu Leu Tyr Tyr 115	120	125	
Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr 130	135	140	

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
 145 150 155 160  
 Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val  
 165 170 175  
 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
 180 185 190  
 Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
 195 200 205  
 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly  
 210 215 220  
 Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys  
 225 230 235 240  
 Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys  
 245 250 255  
 Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
 260 265 270  
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
 275 280 285  
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr  
 290 295 300  
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
 305 310 315 320  
 Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His  
 325 330 335  
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
 340 345 350  
 Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln  
 355 360 365  
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met  
 370 375 380  
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
 385 390 395 400  
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
 405 410 415  
 Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu  
 420 425 430  
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
 435 440 445  
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
 450 455 460

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
465 470

<210> 51  
<211> 236  
<212> PRT  
<213> Homo sapiens

<400> 51  
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp  
1 5 10 15

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Phe Thr Cys Arg Ala Ser  
35 40 45

Gln Asp Ile Arg Arg Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys  
50 55 60

Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Arg Leu Gln Ser Gly Val  
65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr  
85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln  
100 105 110

His Asn Asn Tyr Pro Arg Thr Phe Gly Gln Gly Thr Glu Val Glu Ile  
115 120 125

Ile Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

<210> 52  
<211> 236  
<212> PRT  
<213> Homo sapiens

<400> 52  
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
   1               5                           10                           15  
 Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
   20              25   30  
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
   35              40   45  
 Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys  
   50              55   60  
 Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val  
   65              70   75                           80  
 Pro Ser Arg Phe Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr  
   85              90   95  
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln  
   100            105   110  
 His Asn Ser Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
   115            120   125  
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
   130            135   140  
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
   145            150   155                           160  
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
   165            170   175  
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
   180            185   190  
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
   195            200   205  
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
   210            215   220  
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
   225            230   235  
  
 <210> 53  
 <211> 326  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Consensus  
       sequence  
  
 <220>  
 <221> modified\_base  
 <222> (289)

<223> a, c, t, g, other or unknown

<400> 53  
gacatccaga tgacctcagty tccatcctcc ctgtctgcat ctgttaggaga cagagtcacc 60  
wtcaacttgcc gggcaagtca ggrcattaga mrtgatttag gctggwtca gcagaaacca 120  
ggaaaagcyc ctaagcgcct gatctatgct gcatccmrwt trcammgwgg ggtcccatca 180  
agtttcagcg gcagtggatc tggacagaa ttcaactctca caatcagcmg cctgcagcct 240  
gaagattttg caacttatta ctgttytacar cataatartt aycckybsns ktttygcsrr 300  
gggaccrags tgaratcaw acgaac 326

<210> 54  
<211> 322  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus sequence

<400> 54  
gacatccaga tgacctcagtc tccatcctcc ctgtctgcat ctgyaggaga cagagtcacc 60  
atcaacttgcc gggcaagtca gagcattagy asctwttaa attggtatca gcagaaacca 120  
ggaaaagccc ctaarctcct gatcyatgyt gcatcoagtt trcaargtg ggtcccatca 180  
agtttcagtg gcagtggatc tggacagat ttcaactctca ccatacagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacartr ccccaaychc ttgcggcga 300  
gggaccaagg tggagatcaa ac 322

<210> 55  
<211> 325  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus sequence

<220>  
<221> modified\_base  
<222> (291)  
<223> a, c, t, g, other or unknown

<400> 55  
gaaatttgtt tgacgcagtc tccaggcacc ctgtctttgt ctccaggggaa aagagccacc 60  
ctctcctgya gggccagtc gaggtttmgc rgcagstact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggtc cctcatctat ggtgcattcca gcagggccac tggcatcccc 180  
gacaggttca gtggcagttgg gttctggaca gacttcaactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagttgtw ttactgtcag cagttatggta gytcacctcs nacgttcggc 300  
caagggacca aggtggaaat caaac 325

<210> 56  
<211> 376  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus sequence

<400> 56  
caggtgcagc tgggtggagtc tgggggaggc ttggtaaagc ctggagggtc cctgagactc 60  
tcctgtcgac cctctggatt cacyytcagt gactactaya ttagctggat ccggccaggct 120  
ccagggaagg ggctggartg ggtttcatac attagtagta gtggtagtac cakakactac 180  
gcagactctg tgaaggccc attcaccatc tccaggaca acggcaagaa ctcactgtat 240  
ctgcaaatacga acagcctgag agccgaggac acggccgtgt attactgtgy gagagatgga 300  
gtggaaaacta ctttttacta ctactactac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctcag 376

<210> 57  
<211> 358  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus sequence

<220>  
<221> modified\_base  
<222> (337)  
<223> a, c, t, g, other or unknown

<400> 57  
caggtgcagc tgcaggagtc gggcccagga ctggtaaagc cttcgagac cctgtccctc 60  
acctgcactg tctctgggtt ctccatca gtttacttggat ccggcagccc 120  
gccgggaagg gactggagtg gattggcggt atctatacca gtgggagcmc caactacaac 180  
ccctccctca agagtcgagt caccatgtca gtagacacgt ccaagaacca gttctccctg 240  
aagctgarct ctgtgaccgc cgccggacacg gccgtgtatt actgtgcggt aacgattttt 300  
ggagtggta ttatcttga ctactggggc cagrganccc tggtcacccgt ctcctcag 358

<210> 58  
<211> 418  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus sequence

<400> 58  
caggtgcagc tgggtggagtc tgggggaggc ttggtaaagc ctggggggtc cctgagactc 60  
tcctgtcrag cctctggatt cacctttagc agctatgcca tgarctgggt ccggccaggct 120  
ccagggaagg ggctggagtg ggtctcagst attastggka gtggtaggtab yacatwctac 180  
gcagactccg tgaaggccc gttcaccatc tccagagaca attccargam cacgctgtat 240  
ctgcaaatacga acagcctgag agccgaggac acggccgtat attactgtgc gaaagatctk 300  
ggctrsksysg actyttacta ctactactac ggtatggacg tctggggcca agggacyacg 360  
gtgattatga gttgggttcga cccctggggc cagggaaaccc tggtcacccgt ctcctcag 418

<210> 59  
<211> 364  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus

sequence

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<400> 59
caggtgcagc tgcaggagtc gggcccagga ctggtaaagc cttcgagac cctgtccctc 60
actgtcaact tctctggggg ctccatcagt atttactact ggagytggat ccggcagccc 120
ccaggaaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180
ccctccctca agagtcgact caccatatca gtagacacgt ccaagaacca gttctccctg 240
aagctgagyt ctgtgaccgc tgccggacacg gccgtgtatt actgtgccag gacgtatagc 300
agttcgttct actactacgg tatggacgtc tggggccaag ggaccacggc caccgtctcc 360
tcag
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<210> 60

<211> 15

<212> PRT

### <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gly-Ser Linker

<400> 60

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15